## SEQUENCE LISTING

- <110> Reed, John C.
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  Oliveira, Vasco A.
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  Pawlowski, Krzysztof
- <120> Card3X-2 Polypeptides, Encoding Nucleic Acids, and Methods of Use
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- <151> 2000-05-24
- <150> US 09/686,347
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- <150> US 60/275,980
- <151> 2001-03-14
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Lys Leu Leu Glu Ile Leu Gln His Asp Pro Asp Ser Ile Leu Asp Thr
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Ile Thr Asp Asp Leu Phe Val Trp Asn Val Leu Asn Arg Glu Glu Val
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40 45 50

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890 895 900

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Asp	Бец	тър	100	neu	AIG	GIII	АЗР		_		Leu		110	1111	110
Ser	Phe	Leu		Phe	Tvr	Pro	Leu							Ile	Phe
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~1 <u>~</u>	Dha	275	71.	T ~~~	mh -a	77 -	280		<b>~1</b>			285	~1.,	7 an	Com
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712		λla	T 011	Tla	λνα		₹7 <b>5</b> ]	Lau	т1а	Larg		T.OU	λΊэ	Glu	Gl v
305	GIII	AIA	шец	116	310	GIU	var.	пец	110	315	Giu	Leu	ліа	Gra	320
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~1 <u>~</u>	7	Dha	420	Dage	T	Ma ess	T	425	Dha	:	T	Com	430	<u>ما</u> ت	<b>C1.</b>
GIII	Arg	435	ьуѕ	Pro	гух	Tyr	ьуs 440	Pne	Pne	птр	гÀв	445	Pne	Gln	GIU
Тагт	Thr		Cl w	λνα	λνα	Lau		Car	T.011	: T.O.1	Thr		шie	Glu	Dro
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Ser	Ser	Val	Glu		Thr	Arg	Ala	Val		Lys	His	Leu	Ala	Ala	Val
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                         45
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90 95 100

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Tyr Ile Val Lys Ser Leu Ser Ser Glu Pro Cys Asp Leu Glu Glu Ile													
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Gln Asn Leu His Asn Leu Val Lys Leu Ser Ile Leu Asp Leu Ser Glu 180 185 190													
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230

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Ile Thr Asp Asp Leu Phe Val Trp Asn Val Leu Asn Arg Glu Glu Val
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Asn Ile Ile Cys Cys Glu Lys Val Glu Gln Asp Ala Ala Arg Gly Ile
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att cac atg att ttg aaa aag ggt tca gag tcc tgt aac ctc ttt ctt
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Ile His Met Ile Leu Lys Lys Gly Ser Glu Ser Cys Asn Leu Phe Leu
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25 30 35

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						aac Asn										534
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 Arg
 Arg
 Arg
 Ile
 Lys
 Arg
 Arg</th

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Leu	Leu	His		Thr	Pro	Pro	Asp		Ala	Ser	GIn	Gly		Gly	Pro
_	_	_	500		_	_	_	505	_	_	•		510		-
Ser	Leu		Arg	GIY	Arg	Leu		Thr	Leu	Leu	HIS		GIĀ	Arg	Leu
77.	Leu	515	<b>~1</b>	T 011	c1	Mot	520	Crra	TT 220	1701	Dho	525	ת דת	Cln	Cln
Ата	530	пр	GTÀ	пеп	GIY	535	Cys	Cys	TYL	vaı	540	SEL	AIA	GIII	GIII
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625	Glu	Dro	ui c	7 cn	630 Lou	Gln	Tla	Thr	בות		Dhe	T.011	λla	Gl v	
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T.e.11	Asn	Val	G] v		T.em	Lvs	T.e.ii	Thr		Cvs	Ser	Va1	Glv		Thr
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Cys	Glu	GIn		Gin	ьуs	Leu	Ата		GIY	Asn	Asn	Tyr		Thr	Ата
- רמ	Gly	7 l =	820 Gln	V=7	Len	<b>Δ</b> Ι =	۱۰۱ ای	825	Len	Δνα	Gl v	Δen	830 Thr	Ser	T.eu
AId	GIA	835	GTII	vai	ьси	ATA	840	GIY	neu	~r.A	GTÅ	845	1111	DET	Leu
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Glu Ile Leu Gln His Asp Pro Asp Ser Ile Leu Asp Thr Leu Thr Ser
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Arg Arg Leu Ile Ser Glu Glu Glu Tyr Glu Thr Leu Glu Asn Val Thr
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Asp Leu Leu Lys Lys Ser Arg Lys Leu Leu Ile Leu Val Gln Lys Lys
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Leu Leu Ser Trp Glu Val Leu Ser Trp Glu Asp Tyr Glu Gly Phe His
         35
ctc ctg ggc cag cct ctc tcc cac ttg gcc agg cgc ctt ctg gac acc
                                                                   192
Leu Leu Gly Gln Pro Leu Ser His Leu Ala Arg Arg Leu Leu Asp Thr
     50
                                             60
                         55
gtc tgg aat aag ggt act tgg gcc tgt cag aag ctc
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Val Trp Asn Lys Gly Thr Trp Ala Cys Gln Lys Leu
 65
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<210> 170

<211> 76

<212> PRT

<213> Homo sapiens <400> 170 Met Cys Ser Gln Glu Ala Phe Gln Ala Gln Arg Ser Gln Leu Val Glu 10 Leu Leu Val Ser Gly Ser Leu Glu Gly Phe Glu Ser Val Leu Asp Trp 25 Leu Leu Ser Trp Glu Val Leu Ser Trp Glu Asp Tyr Glu Gly Phe His Leu Leu Gly Gln Pro Leu Ser His Leu Ala Arg Arg Leu Leu Asp Thr Val Trp Asn Lys Gly Thr Trp Ala Cys Gln Lys Leu 70 <210> 171 <211> 243 <212> DNA <213> Homo sapiens <220> <221> CDS <222> (1) ... (243) <400> 171 cca gcc cga gac ctg cag agt cac cgg cca gcc att gtc agg agg ctc Pro Ala Arg Asp Leu Gln Ser His Arg Pro Ala Ile Val Arg Arg Leu 10 cac agc cat gtg gag aac atg ctg gac ctg gca tgg gag cgg ggt ttc His Ser His Val Glu Asn Met Leu Asp Leu Ala Trp Glu Arg Gly Phe 20 25 gtc agc cag tat gaa tgt gat gaa atc agg ttg ccg atc ttc aca ccg Val Ser Gln Tyr Glu Cys Asp Glu Ile Arg Leu Pro Ile Phe Thr Pro

144

96

tcc cag agg gca aga agg ctg ctt gat ctt gcc acg gtg aaa gcg aat 192 Ser Gln Arg Ala Arg Arg Leu Leu Asp Leu Ala Thr Val Lys Ala Asn 50 55

gga ttg gct gcc ttc ctt cta caa cat gtt cag gaa tta cca gtc cca 240 Gly Leu Ala Ala Phe Leu Leu Gln His Val Gln Glu Leu Pro Val Pro 75 80 65 70

ttg 243 Leu

<210> 172 <211> 81

<212> PRT

## <213> Homo sapiens

<400> 172 Pro Ala Arg Asp Leu Gln Ser His Arg Pro Ala Ile Val Arg Arg Leu 10 His Ser His Val Glu Asn Met Leu Asp Leu Ala Trp Glu Arg Gly Phe 🥆 Val Ser Gln Tyr Glu Cys Asp Glu Ile Arg Leu Pro Ile Phe Thr Pro Ser Gln Arg Ala Arg Leu Leu Asp Leu Ala Thr Val Lys Ala Asn Gly Leu Ala Ala Phe Leu Leu Gln His Val Gln Glu Leu Pro Val Pro 70 Leu <210> 173 <211> 888 <212> DNA <213> Homo sapiens <220> <221> CDS <222> (1) ... (888) <400> 173 gac gat gcg gac act gtg ctg gtg gtg ggt gag gcg ggc agt ggc aag Asp Asp Ala Asp Thr Val Leu Val Val Gly Glu Ala Gly Ser Gly Lys 1 age acg etc etg eag egg etg eac ttg etg tgg get gea ggg eaa gae Ser Thr Leu Leu Gln Arg Leu His Leu Leu Trp Ala Ala Gly Gln Asp 20 ttc cag gaa ttt ctc ttt gtc ttc cca ttc agc tgc cgg cag ctg cag 144 Phe Gln Glu Phe Leu Phe Val Phe Pro Phe Ser Cys Arg Gln Leu Gln 35 tgc atg gcc aaa cca ctc tct gtg cgg act cta ctc ttt gag cac tgc 192 Cys Met Ala Lys Pro Leu Ser Val Arg Thr Leu Leu Phe Glu His Cys 55 50 60 tgt tgq cct gat gtt ggt caa gac atc ttc cag tta ctc ctt gac 240 Cys Trp Pro Asp Val Gly Gln Glu Asp Ile Phe Gln Leu Leu Asp 65 70 75 80 cac cct gac cgt gtc ctg tta acc ttt gat ggc ttt gac gag ttc aag 288 His Pro Asp Arg Val Leu Leu Thr Phe Asp Gly Phe Asp Glu Phe Lys 85 tte agg tte acg gat egt gaa ege cae tge tee eeg ace gac eec ace 336

Phe Arg Phe Thr Asp Arg Glu Arg His Cys Ser Pro Thr Asp Pro Thr

100 105 110

	_	_	_	ctc Leu				_	-			_	_	_	384
				gtg Val		-									432
				cgc Arg 150											480
_			 _	tac Tyr	_		_	_							528
	_	-		cgc Arg	_						_				576
_	-			gtc Val				_				-		-	624
				gag Glu											672
	_	-	-	cag Gln 230			_	_		_					720
	-			ctg Leu			_					-			768
				ggc Gly											816
				gcc Ala											864
_	-			ggc Gly		-									888

<210> 174 <211> 296

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<213> Homo sapiens
<400> 174
Asp Asp Ala Asp Th
1 5
Ser Thr Leu Leu Gl
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295

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													cca Pro			144
		_	_		_	_		_	_			-	ctg Leu		_	192
			-		_						Pro		ctt Leu			240
	_					_		_		_	_	-	ctg Leu			288
													cag Gln 110			336
_	_	_		-	_								cgt Arg			384
					_								cac His			432
													gct Ala			480
													cca Pro			528
		_	_			_		_	_	_		_	gcc Ala 190	-		576
													gag Glu			624

	c ctt n Leu 210	_			_	-		-	-		_	_				672
	c tgg s Trp 5		_	_	_		_	_			-	_	_	_		720
_	g cgc g Arg	_	_	_	-	-		_	_	_	_	_		_	_	768
	c ttc s Phe				_		_	_	_				_	_		816
	t gcc s Ala	_									_	_				864
	g gag n Glu 290	Glu														912
	.c ctc .s Leu 5	_	_			_	_					-	_	_	-	960
	g gcc u Ala			_	_						_	_		_	_	1008
_	c tac p Tyr					-						_	_		-	1056
	t ggt u Gly	_	_	_	_	_		_	_	_					-	1104
	a ggc g Gly 370															1152
	g aag n Lys 5			_										_		1200
	g ctg l Leu															1209

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<210> 176
<211> 403
<212> PRT
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355 360 365 Arg Gly Ile Cys Lys Leu Ile Glu Cys Ala Leu His Cys Glu Gln Leu

370 Gln Lys Leu Ala 385 Val Leu Ala	379 Leu Gly Asi 390			380 Ala Ala G	Sly Ala	Gln 400
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<220> <221> CDS <222> (1)(261	1)					
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atg act gtt ata Met Thr Val Ile 20	_	_	_	-		_
ctg aat cgc gaa Leu Asn Arg Glu 35	-		-			
gat gct gct aga Asp Ala Ala Arg 50		e His Met				
tcc tgt aac ctc Ser Cys Asn Leu 65						
ttt cag gac ttg Phe Gln Asp Leu						261
<210> 178 <211> 87 <212> PRT <213> Homo sapie	ens					
<400> 178						
Met Asn Phe Ile	5		10		15	
Met Thr Val Ile 20	-	25		3	30	
Leu Asn Arg Glu	GIU VAI AS	i iie iie	cys cys (	сти гуз /	ar GIU	GTII

45

40

35

Asp Ala Ala Arg Gly Ile Ile His Met Ile Leu Lys Lys Gly Ser Glu Ser Cys Asn Leu Phe Leu Lys Ser Leu Lys Glu Trp Asn Tyr Pro Leu 75 Phe Gln Asp Leu Asn Gly Gln 85 <210> 179 <211> 891 <212> DNA <213> Homo sapiens <220> <221> CDS <222> (1) ... (891) <400> 179 ctt cag agc ccc tgc atc att gaa ggg gaa tct ggc aaa ggc aag tcc Leu Gln Ser Pro Cys Ile Ile Glu Gly Glu Ser Gly Lys Gly Lys Ser act ctg ctg cag cgc att gcc atg ctc tgg ggc tcc gga aag tgc aag Thr Leu Leu Gln Arg Ile Ala Met Leu Trp Gly Ser Gly Lys Cys Lys 25 get etg ace aag tte aaa tte gte tte tte ete egt ete age agg gee 144 Ala Leu Thr Lys Phe Lys Phe Val Phe Phe Leu Arg Leu Ser Arg Ala 35 cag ggt gga ctt ttt gaa acc ctc tgt gat caa ctc ctg gat ata cct 192 Gln Gly Gly Leu Phe Glu Thr Leu Cys Asp Gln Leu Leu Asp Ile Pro 50 55 ggc aca atc agg aag cag aca ttc atg gcc atg ctg ctg aag ctg cgg 240 Gly Thr Ile Arg Lys Gln Thr Phe Met Ala Met Leu Leu Lys Leu Arg cag agg gtt ctt ttc ctt ctt gat ggc tac aat gaa ttc aag ccc cag 288 Gln Arg Val Leu Phe Leu Leu Asp Gly Tyr Asn Glu Phe Lys Pro Gln 85 90 aac tgc cca gaa atc gaa gcc ctg ata aag gaa aac cac cgc ttc aag 336 Asn Cys Pro Glu Ile Glu Ala Leu Ile Lys Glu Asn His Arg Phe Lys 100 105 aac atg gtc atc gtc acc act acc act gag tgc ctg agg cac ata cgg 384 Asn Met Val Ile Val Thr Thr Thr Glu Cys Leu Arg His Ile Arg 120 cag ttt ggt gcc ctg act gct gag gtg ggg gat atg aca gac agc 432

Gln Phe Gly Ala Leu Thr Ala Glu Val Gly Asp Met Thr Glu Asp Ser

130 135 140

											gag Glu				480
_	_				-				_		agg Arg			-	528
					_			_	_		cag Gln				576
								_	_		cat His				624
_	_		_								ggt Gly 220	-			672
_				_	_	_		-		_	cta Leu	_			720
											gat Asp				768
											tgt Cys				816
			_		_						aag Lys		_		864
		_		_	aga Arg		_	_							891
	0> 10 1> 20						•								

<212> PRT

<213> Homo sapiens

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Ala Leu Thr Lys Phe Lys Phe Val Phe Phe Leu Arg Leu Ser Arg Ala

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Gln Gly Gly Leu Phe Glu Thr Leu Cys Asp Gln Leu Leu Asp Ile Pro
Gly Thr Ile Arg Lys Gln Thr Phe Met Ala Met Leu Leu Lys Leu Arg
                    70
                                        75
Gln Arg Val Leu Phe Leu Leu Asp Gly Tyr Asn Glu Phe Lys Pro Gln
                85
                                    90
Asn Cys Pro Glu Ile Glu Ala Leu Ile Lys Glu Asn His Arg Phe Lys
                                105
Asn Met Val Ile Val Thr Thr Thr Glu Cys Leu Arg His Ile Arg
                            120
Gln Phe Gly Ala Leu Thr Ala Glu Val Gly Asp Met Thr Glu Asp Ser
                        135
Ala Gln Ala Leu Ile Arg Glu Val Leu Ile Lys Glu Leu Ala Glu Gly
                    150
Leu Leu Gln Ile Gln Lys Ser Arg Cys Leu Arg Asn Leu Met Lys
                                    170
Thr Pro Leu Phe Val Val Ile Thr Cys Ala Ile Gln Met Gly Glu Ser
                                185
Glu Phe His Ser His Thr Gln Thr Thr Leu Phe His Thr Phe Tyr Asp
        195
                            200
Leu Leu Ile Gln Lys Asn Lys His Lys His Lys Gly Val Ala Ala Ser
                        215
Asp Phe Ile Arg Ser Leu Asp His Arg Gly Asp Leu Ala Leu Glu Gly
                    230
                                        235
Val Phe Ser His Lys Phe Asp Phe Glu Leu Gln Asp Val Ser Ser Val
                                    250
                245
Asn Glu Asp Val Leu Leu Thr Thr Gly Leu Leu Cys Lys Tyr Thr Ala
                                265
                                                    270
Gln Arg Phe Lys Pro Lys Tyr Lys Phe Phe His Lys Ser Phe Gln Glu
                            280
Tyr Thr Ala Gly Arg Arg Leu Ser Ser
                        295
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Gly Asn Leu Lys Asn Leu Thr Lys Leu Ile Met Asp Asn Ile Lys Met
 1
                                                          15
                 5
                                     10
aat gaa gaa gat gct ata aaa cta gct gaa ggc ctg aaa aac ctg aag
Asn Glu Glu Asp Ala Ile Lys Leu Ala Glu Gly Leu Lys Asn Leu Lys
             20
                                                      30
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_	_	_			ttg Leu		-		_		_	_	144
_					tct Ser 55								192
					tgc Cys								240
					aat Asn								288
	_		_	_	aaa Lys	_							336
					cta Leu								384
					ggc Gly 135								432
		_			gtc Val	_		_			_		480
	_			_	att Ile		 _			_			528
					ttg Leu								576
_			_		atg Met								618

<210> 182

<211> 206 .

<212> PRT

<213> Homo sapiens

Gly Asn Leu Lys Asn Leu Thr Lys Leu Ile Met Asp Asn Ile Lys Met Asn Glu Glu Asp Ala Ile Lys Leu Ala Glu Gly Leu Lys Asn Leu Lys Lys Met Cys Leu Phe His Leu Thr His Leu Ser Asp Ile Gly Glu Gly 40 Met Asp Tyr Ile Val Lys Ser Leu Ser Ser Glu Pro Cys Asp Leu Glu 55 Glu Ile Gln Leu Val Ser Cys Cys Leu Ser Ala Asn Ala Val Lys Ile 70 Leu Ala Gln Asn Leu His Asn Leu Val Lys Leu Ser Ile Leu Asp Leu 90 Ser Glu Asn Tyr Leu Glu Lys Asp Gly Asn Glu Ala Leu His Glu Leu 105 Ile Asp Arg Met Asn Val Leu Glu Gln Leu Thr Ala Leu Met Leu Pro 120 Trp Gly Cys Asp Val Gln Gly Ser Leu Ser Ser Leu Leu Lys His Leu 135 Glu Glu Val Pro Gln Leu Val Lys Leu Gly Leu Lys Asn Trp Arg Leu 150 155 Thr Asp Thr Glu Ile Arg Ile Leu Gly Ala Phe Phe Gly Lys Asn Pro 165 170 Leu Lys Asn Phe Gln Gln Leu Asn Leu Ala Gly Asn Arg Val Ser Ser 185 Asp Gly Trp Leu Ala Phe Met Gly Val Phe Glu Asn Leu Lys 195 200 <210> 183 <211> 165 <212> DNA <213> Homo sapiens <220> <221> CDS <222> '(1) ... (165) <400> 183 acc tac att ccc agc agg gct gta tct ttg ttc ttc aac tgg aag cag Thr Tyr Ile Pro Ser Arg Ala Val Ser Leu Phe Phe Asn Trp Lys Gln gaa ttc agg act ctg gag gtc aca ctc cgg gat ttc agc aag ttg aat 96 Glu Phe Arg Thr Leu Glu Val Thr Leu Arg Asp Phe Ser Lys Leu Asn 20 25 aag caa gat atc aga tat ctg ggg aaa ata ttc agc tct gcc aca agc 144 Lys Gln Asp Ile Arg Tyr Leu Gly Lys Ile Phe Ser Ser Ala Thr Ser 35 40 45 ctc agg ctg caa ata aag aga 165

Leu Arg Leu Gln Ile Lys Arg

50

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<210> 184
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Glu Phe Arg Thr Leu Glu Val Thr Leu Arg Asp Phe Ser Lys Leu Asn
                                 25
Lys Gln Asp Ile Arg Tyr Leu Gly Lys Ile Phe Ser Ser Ala Thr Ser
                             40
Leu Arg Leu Gln Ile Lys Arg
    50
<210> 185
<211> 19
<212> DNA
<213> Artificial Sequence
<220>
<223> primer
<400> 185
                                                                    19
gaaatgtgct cgcaggagg
<210> 186
<211> 20
<212> DNA
<213> Artificial Sequence
<220>
<223> primer
<400> 186
                                                                    20
gatgagcttc tgacaggccc
<210> 187
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<222> (2389)...(2928)
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												gag Glu				96
_			-									gac Asp 45				144
			_		_					_		agg Arg				192
-		_			_				_	_	_	aag Lys			_	240
-	-		-	_	_	-	_	_	-			aag Lys				288
_		_			_				-	_	_	ctg Leu	_	_		336
		_		_								gag Glu 125				384
												gaa Glu				432
		_	_				_		_		_	aga Arg		_		480
												ttc Phe				528
												ttg Leu				576
	-	_	_		_	_	_	_			_	gtg Val 205		_		624
tct	cgc	ttç	ctc	agt	acc	tat	gat	gga	gca	gag	acg	ctc	tgc	ctg	gag	672

Ser	Arg 210	Phe	Leu	Ser	Thr	Tyr 215	Asp	Gly	Ala	Glu	Thr 220	Leu	Cys	Leu	Glu	
_	ata Ile					-										720
	gga Gly															768
	agc Ser							_	_		_			_		816
	ggt Gly				_		_	_	_		_	_		-		864
_	ctg Leu 290		_	_			_		-	_				_		912
	ttc Phe	_	_		_	_	_	_	_	-						960
	act Thr						_	_			_					1008
_	atc Ile		_				_			-	-	_	_			1056
	gat Asp			_			_				_			_		1104
	tgc Cys 370		_		_				_	_		_				1152
	ctg Leu	_			-	_			_	-	_	-	-			1200
	ccg Pro															1248
	aac Asn		_				_	-	-					_		1296

420 425 430

		gag ccc Glu Pro	Gly V								1344
	Thr Sei	a gcc ctg Ala Lei	-	_	_		_		-		1392
		c aaa tgo c Lys Cys 470	His G								1440
	_	c act aca Thr Thr 485	-	-	_	_		_	-		1488
-	_	acc ccc Thr Pro	_		_				_		1536
		g ggc cgc g Gly Arg	Leu P								1584
_	Trp Gly	c ctg ggd / Leu Gl	_			-					1632
		a cag gto a Gln Val 550	Ser P								1680
_		a ggt gto s Gly Val 565									1728
		ttc cag Phe Glr									1776
		g cca cca L Pro Pro	Ala L	_	_					_	 1824
	Gly Ası	c tca cca n Ser Pro									1872
		g gga aag 1 Gly Lys 630	Asp S								1920

gcc gag c Ala Glu F	Pro His A		-		-	_		_	-		_	1968
ttg tcc c Leu Ser A				_	_		_	_			-	2016
aag gcc c Lys Ala I 6				Cys								2064
agc ctc c Ser Leu A 690	-				_							2112
gcc aag a Ala Lys S 705		_	-								_	2160
ctg tac g Leu Tyr G	Glu Met (			-								2208
ctg aat g Leu Asn V			-			_	_					2256
gag tgt g Glu Cys A				Leu								2304
gcc ctg c Ala Leu G 770		_				-		(				2352
ctg ctg c Leu Leu F 785										ggc Gly 1		2400
aga gtg g Arg Val G 800												2448
cac cag a His Gln S	Ser Leu I											2496
gtg ggt g Val Gly A			-									2544

_			gat gaa ggt gta tgt Asp Glu Gly Val Cys 860	2592
			ttg aaa atc ctg aac Leu Lys Ile Leu Asn 875	2640
			ttg gaa agc att ttc Leu Glu Ser Ile Phe 895	2688
			cag aaa gtt gtc aag Gln Lys Val Val Lys 910	2736
			gtc agg ttg tcc aat Val Arg Leu Ser Asn 925	2784
			ctg cag gcc ctt gaa Leu Gln Ala Leu Glu 940	2832
			ggg aac act ttc tct Gly Asn Thr Phe Ser 955	2880
	-		e acc aga ctc ttg ctt o Thr Arg Leu Leu Leu 975	2928
	acatgt gttgg		gcaggctgtg agtttgggcc gagccctgtc ctgcctaagg	
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1	5	10	15 Phe Glu Ser Val Leu	
. 20	_	25	30	
35	-	40	O Glu Asp Tyr Glu Gly 45	
50	55		ı Ala Arg Arg Leu Leu 60	
Asp Thr Val Trp	Asn Lys Gly 70	Thr Trp Ala Cys	Gln Lys Leu Ile Ala 80	
Ala Ala Gln Glu	Ala Gln Ala	Asp Ser Gln Ser	Pro Lys Leu His Gly	

				85					90					95	
Cys	Trp	Asp	Pro 100	His	Ser	Leu	His	Pro 105	Ala	Arg	Asp	Leu	Gln 110	Ser	His
Arg	Pro	Ala 115		Val	Arg	Arg	Leu 120	His	Ser	His	Val	Glu 125	Asn	Met	Leu
Asp	Leu 130		Trp	Glu	Arg	Gly 135		Val	Ser	Gln	Tyr 140		Cys	Asp	Glu
Ile 145		Leu	Pro	Ile	Phe 150		Pro	Ser	Gln	Arg 155		Arg	Arg	Leu	Leu 160
	Leu	Ala	Thr		Lys	Ala	Asn	Gly			Ala	Phe	Leu		
His	Val	Gln		165 Leu	Pro	Val	Pro		170 Ala	Leu	Pro	Leu		175 Ala	Ala
Thr	Cys		180 Lys	Tyr	Met	Ala		185 Leu	Arg	Thr	Thr		190 Ser	Ala.	Gln
Ser	_	195 Phe	Leu	Ser	Thr		200 Asp	Gly	Ala	Glu		205 Leu	Cys	Leu	Glu
_	210 Ile	Tyr	Thr	Glu	Asn	215 Val	Leu	Glu	Val	_	220 Ala	Asp	Val	Gly	
225 Ala	Gly	Pro	Pro	Gln 245	230 Lys	Ser	Pro	Ala	Thr 250	235 Leu	Gly	Leu	Glu	Glu 255	240 Leu
Phe	Ser	Thr	Pro 260		His	Leu	Asn	Asp 265		Ala	Asp	Thr	Val 270		Val
Val	Gly	Glu 275		Gly	Ser	Gly	Lys 280		Thr	Leu	Leu	Gln 285		Leu	His
Leu	Leu 290		Ala	Ala	Gly	Gln 295	Asp	Phe	Gln	Glu	Phe		Phe	Val	Phe
Pro 305		Ser	Cys	Arg	Gln 310		•	Cys	Met	Ala 315		Pro	Leu	Ser	Val
	Thr	Leu		Phe .325	Glu	His	Cys	Cys	Trp 330		Asp	Val	Gly	Gln 335	
Asp	Ile	Phe			Leu	Leu	Asp	His		Asp	Arg	Val	Leu 350		Thr
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His	Cys 370		Pro	Thr	Asp	Pro 375		Ser	Val	Gln	Thr 380		Leu	Phe	Asn
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Lys	Arg	His		Glu	Pro	Gly	Val 440		Asp	Arg	Leu	Ile 445		Leu	Leu
Gln	Glu 450		Ser	Ala	Leu	His		Leu	Cys	His	Leu 460		Val	Phe	Ser
Trp 465		Val	Ser	Lys	Cys 470		Gln	Glu	Leu	Leu 475		Gln	Glu	Gly	Gly 480
	Pro	Lys	Thr	Thr 485	Thr	Asp	Met	Tyr	Leu 490		Ile	Leu	Gln	His 495	
Leu	Leu	His	Ala 500		Pro	Pro	Asp	Ser 505		Ser	Gln	Gly	Leu 510		Pro

Ser Leu Leu Arg Gly Arg Leu Pro Thr Leu Leu His Leu Gly Arg Leu 520 Ala Leu Trp Gly Leu Gly Met Cys Cys Tyr Val Phe Ser Ala Gln Gln 535 540 Leu Gln Ala Ala Gln Val Ser Pro Asp Asp Ile Ser Leu Gly Phe Leu 550 555 Val Arg Ala Lys Gly Val Val Pro Gly Ser Thr Ala Pro Leu Glu Phe 565 570 Leu His Ile Thr Phe Gln Cys Phe Phe Ala Ala Phe Tyr Leu Ala Leu 585 Ser Ala Asp Val Pro Pro Ala Leu Leu Arg His Leu Phe Asn Cys Gly 600 Arg Pro Gly Asn Ser Pro Met Ala Arg Leu Leu Pro Thr Met Cys Ile 615 620 Gln Ala Ser Glu Gly Lys Asp Ser Ser Val Ala Ala Leu Leu Gln Lys 630 635 Ala Glu Pro His Asn Leu Gln Ile Thr Ala Ala Phe Leu Ala Gly Leu 645 650 Leu Ser Arg Glu His Trp Gly Leu Leu Ala Glu Cys Gln Thr Ser Glu 665 Lys Ala Leu Leu Arg Arg Gln Ala Cys Ala Arg Trp Cys Leu Ala Arg 680 Ser Leu Arg Lys His Phe His Ser Ile Pro Pro Ala Ala Pro Gly Glu 695 Ala Lys Ser Val His Ala Met Pro Gly Phe Ile Trp Leu Ile Arg Ser 710 715 Leu Tyr Glu Met Gln Glu Glu Arg Leu Ala Arg Lys Ala Ala Arg Gly 725 730 Leu Asn Val Gly His Leu Lys Leu Thr Phe Cys Ser Val Gly Pro Thr 740 745 Glu Cys Ala Ala Leu Ala Phe Val Leu Gln His Leu Arg Arg Pro Val 760 Ala Leu Gln Leu Asp Tyr Asn Ser Val Gly Asp Ile Gly Val Glu Gln 775 \ Leu Leu Pro Cys Leu Gly Val Cys Lys Ala Leu 790

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Lys Val Val Lys Ile Leu Glu Glu Met Val Val Ser Trp Leu Glu Val
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Arg Leu Ser Asn Asn Cys Ile Thr Tyr Leu Gly Ala Glu Ala Leu Leu
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Asn Thr Phe Ser Leu Glu Glu Val Asp Lys Leu Gly Cys Arg Asp Thr
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gaagcagccc tg ctg cag aag gct gag cca cac aac ctg caa atc aca gca 231
              Leu Gln Lys Ala Glu Pro His Asn Leu Gln Ile Thr Ala
ged tto cta gca ggt ctg ttg tcc cag cat cgg gad ctg ttg gct
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Ala Phe Leu Ala Gly Leu Leu Ser Gln Gln His Arg Asp Leu Leu Ala
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Ala Cys Gln Val Ser Glu Arg Val Leu Leu Gln Arg Gln Ala Arg Ala
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ege teg tgt etg gee cae age ete ege gag cae tte cat tee ate eeg
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Arg Ser Cys Leu Ala His Ser Leu Arg Glu His Phe His Ser Ile Pro
cct gcc gtg ccc ggt gag acc aag agc atg cat gct atg ccg ggc ttc
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Pro Ala Val Pro Gly Glu Thr Lys Ser Met His Ala Met Pro Gly Phe
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                                 70
                                                      75
att tgg ctc atc cgt agc ctg tac gag atg cag gag gag cag ttg gcc
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Ile Trp Leu Ile Arg Ser Leu Tyr Glu Met Gln Glu Gln Leu Ala
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-		_	_		_	cag Gln			_	_	_	_	_	_	_	96
					_	ctc Leu	_	-	_	_	_	_	-	_	_	144
	_					gag Glu 55						_		_		192
		-		_	_	atg Met		_	_	-						240
						atg Met										288
_	_	_	_	_		Gly 333		_	_	_			_	_	-	336
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			_		_	ctg Leu 135	_				gt					419
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Ala	Gly	Leu	Leu 20	Ser	Gln	Gln	His	Arg 25	Asp	Leu	Leu	Ala	Ala 30	Cys	Gln	•
Ile	Ser	Glu 35	Arg	Val	Leu	Leu	Gln 40	Arg	Gln	Ala	Arg	Ala 45	Arg	Ser	Cys	
Leu	Ala 50		Ser	Leu	Arg	Glu 55	His	Phe	His	Ser	Ile 60	Pro	Pro	Ala	Val	
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Leu Leu Val Ser Gly Ser Leu Glu Gly Phe Glu Ser Val Leu Asp Trp
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ctg ctg tcc tgg gag gtc ctc tcc tgg gag gac tac gag ggc ttc cac
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Leu Leu Ser Trp Glu Val Leu Ser Trp Glu Asp Tyr Glu Gly Phe His
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40

35

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														tgc Cys 95		288	
_			_				_	_	-	_				cgg Arg		336	
Ala	Ile	Val	Arg	Arg	Leu	His	Ser 120	His	Val	Glu	Asn	Met 125	Leu	gac Asp	Leu	384	
Ala	Trp 130	Glu	Arg	Gly	Phe	Val 135	Ser	Gln	Tyr	Glu	Cys 140	Asp	Glu	atc Ile	Arg	432	
Leu 145	Pro	Ile	Phe	Thr	Pro 150	Ser	Gln	Arg	Ala	Arg 155	Arg	Leu	Leu	gat Asp	Leu 160	480	
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Gln	Glu	Leu	Pro 180	Val	Pro	Leu	Ala	Leu 185	Pro	Leu	Glu	Ala	Ala 190	aca Thr	Cys	576	
Lys	Lys	Tyr 195	Met	Ala	Lys	Leu	Arg 200	Thr	Thr	Val	Ser	Ala 205	Gln	tct Ser	Arg	624	
Phe	Leu 210	Ser	Thr	Tyr	Asp	Gly 215	Ala	Glu	Thr	Leu	Cys 220	Leu	Glu	gac Asp	Ile	672	
Tyr 225	Thr	Glu	Asn	Val	Leu 230	Glu	Val	Trp	Ala	Asp 235	Val	Gly	Met	gct Ala	Gly 240	720	
Pro	Pro	Gln	Lys	Ser 245	Pro	Ala	Thr	Leu	Gly 250	Leu	Glu	Glu	Leu	Phe 255	Ser	768	
acc	cct	ggc	cac	ctc	aat	gac	gat	gcg	gac	act	gtg	ctg	gtg	gtg	ggt	816	

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Trp	_	_			_		_	-				_	ttc Phe			912
													gtg Val			960
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Ser													aac Asn			1152
											-		agc Ser			1200
													gag Glu			1248
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							-	_				_	ctc Leu			1344
Thr						_	_				-		tca Ser		_	1392
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					tct Ser									:	2352
					tgc Cys 790									:	2400
					tgc Cys									:	2448
					gct Ala									:	2496
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					aac Asn									:	2592
					ggc Gly 870									:	2640
					gac Asp									:	2688

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Leu Leu Gly Gln Pro Leu Ser His Leu Ala Arg Arg Leu Leu Asp Thr 50 55 60	
Val Trp Asn Lys Gly Thr Trp Ala Cys Gln Lys Leu Ile Ala Ala Ala 65 70 75 80	
Gln Glu Ala Gln Ala Asp Ser Gln Ser Pro Lys Leu His Gly Cys Trp 85 90 95	
Asp Pro His Ser Leu His Pro Ala Arg Asp Leu Gln Ser His Arg Pro 100 105 110	

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Pro	His	Asn	Leu	${\tt Gln}$	Ile	Thr	Ala	Ala	Phe	Leu	Ala	Gly	Leu	Leu	Ser
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Arg	g Glu	His	$\mathtt{Trp}$	Gly	Leu	Leu	Ala		Cys	Gln	Thr	Ser	Glu	Lys	Ala
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Let	ı Leu	_	_		Ala	Cys		Arg	Trp	Cys	Leu		Arg	Ser	Leu
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0	690 Val	774 -	77-	N/	Dage	695	Dho	T1.	TT-2000	T 011	700	7 ~~	C 0 20	T 011	П
70!		HIS	Ala	Mec	710	GTÅ	Pne	ire	пр	715	116	Arg	ser	ьеu	720
	, 1 Met	Gln	Glu	Glu		T.A11	Δla	Δra	Lvg		Δla	Δτα	Glv	T.e.11	
GI	ı Mec	GIII	Giu	725	AI 9	пси	AIG	y	730	miu	711.0	9	017	735	11011
Va <sup>-</sup>	lGly	His	Leu		Leu	Thr	Phe	Cvs		Val	Glv	Pro	Thr		Cvs
	- 0-1		740	-1-				745			1		750		- 2
Ala	a Ala	Leu				Leu	Gln	His	Leu	Arq	Arg	Pro	Val	Ala	Leu
							760			_		765			
Gli	ı Leu	Asp	Tyr	Asn	Ser	Val	Gly	Asp	Ile	Gly	Val	Glu	Gln	Leu	Leu
	770					775					780		_		
Pro	Cys	Leu	Gly	Val	Cys	Lys	Ala	Leu	Tyr	Leu	Arg	Asp	Asn	Asn	
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Se	c Asp	Arg	Gly		Cys	Lys	Leu	Ile		Cys	Ala	Leu	His		Glu
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GLı	n Leu	Gln	_	Leu	Ala	Leu	Phe		Asn	Lys	Leu	Thr		GLY	Cys
7.7.			820 Mat			T		825		71		7 an	830 Dho	T 011	ת ת
AL	a His	835	мес	Ата	ьуѕ	Leu	840	Ата	Cys	Arg	GIII	845	PHE	ьeu	Ата
T.A1	ı Arg		Glv	λen	λen	ጥኒፖ		Thr	Δla	Δla	Glv		Gln	Val	T.em
пе	850	шец	Gry	ASII	ASII	855	110	1111	ALG	nia	860	ALU	0111	vai	Leu
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	y Asn	Arq	Val	Gly		Glu	Gly	Ala	Gln		Leu	Ala	Glu	Ala	Leu
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Me	t Leu	Glu	Glu	Leu	Cys	Leu	Glu	Glu	Asn	His	Leu	Gln	Asp	Glu	Gly
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